



SEQUENCE LISTING

<110> WILEY, Steven R.

<120> TWEAK Receptor

<130> 2968-B

<140> US/09/742,454

<141> 2000-12-19

<150> 60/172,878

<151> 1999-12-20

<150> 60/203,347

<151> 2000-05-10

<160> 7

<170> PatentIn Ver. 2.0

<210> 1

<211> 898

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (52)..(873)

<220>

<223> Description of Artificial Sequence: human TWEAK fusion protein construct

<400> 1

tctcgaagggc cacgcgttta aacgtcgagg tacctatccc gggccgccac c atg gct 57
Met Ala
1

aca ggc tcc cgg acg tcc ctg ctc ctg gct ttt ggc ctg ctc tgc ctg 105
Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu
5 10 15

ccc tgg ctt caa gag ggc agt gca act agt tct gac cgt atg aaa cag 153
Pro Trp Leu Gln Glu Gly Ser Ala Thr Ser Ser Asp Arg Met Lys Gln
20 25 30

ata gag gat aag atc gaa gag atc cta agt aag att tat cat ata gag 201
Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu
35 40 45 50

aat gaa atc gcc cgt atc aaa aag ctg att ggc gag cgg act aga tct 249
Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr Arg Ser
55 60 65

agt ttg ggg agc cgg gca tcg ctg tcc gcc cag gag cct gcc cag gag 297
Ser Leu Gly Ser Arg Ala Ser Leu Ser Ala Gln Glu Pro Ala Gln Glu

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<220>

<221> CDS

<222> (52)..(873)

<220>

<223> Description of Artificial Sequence: human TWEAK
fusion protein construct

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1 5 10 15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Thr Ser Ser Asp Arg Met
20 25 30

Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His
35 40 45

Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr
50 55 60

Arg Ser Ser Leu Gly Ser Arg Ala Ser Leu Ser Ala Gln Glu Pro Ala
65 70 75 80

Gln Glu Glu Leu Val Ala Glu Glu Asp Gln Asp Pro Ser Glu Leu Asn
85 90 95

Pro Gln Thr Glu Glu Ser Gln Asp Pro Ala Pro Phe Leu Asn Arg Leu
100 105 110

Val Arg Pro Arg Arg Ser Ala Pro Lys Gly Arg Lys Thr Arg Ala Arg
115 120 125

Arg Ala Ile Ala Ala His Tyr Glu Val His Pro Arg Pro Gly Gln Asp
130 135 140

Gly Ala Gln Ala Gly Val Asp Gly Thr Val Ser Gly Trp Glu Glu Ala
145 150 155 160

Arg Ile Asn Ser Ser Ser Pro Leu Arg Tyr Asn Arg Gln Ile Gly Glu
165 170 175

Phe Ile Val Thr Arg Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val His
180 185 190

Phe Asp Glu Gly Lys Ala Val Tyr Leu Lys Leu Asp Leu Leu Val Asp
195 200 205

Gly Val Leu Ala Leu Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala Ala
210 215 220

Ser Ser Leu Gly Pro Gln Leu Arg Leu Cys Gln Val Ser Gly Leu Leu
225 230 235 240

Ala Leu Arg Pro Gly Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp Ala
245 250 255

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His Leu Lys Ala Ala Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln Val
 260 265 270

His

<210> 3
 <211> 868
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (53)..(442)

<400> 3
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 Met Ala
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cgg ggc tcg ctg cgc cgg ttg ctg cgg ctc ctc gtg ctg ggg ctc tgg 106
 Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly Leu Trp
 5 10 15

ctg gcg ttg ctg cgc tcc gtg gcc ggg gag caa gcg cca ggc acc gcc 154
 Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly Thr Ala
 20 25 30

ccc tgc tcc cgc ggc agc tcc tgg agc gcg gac ctg gac aag tgc atg 202
 Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys Cys Met
 35 40 45 50

gac tgc gcg tct tgc agg gcg cga ccg cac agc gac ttc tgc ctg ggc 250
 Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys Leu Gly
 55 60 65

tgc gct gca gca cct cct gcc ccc ttc cgg ctg ctt tgg ccc atc ctt 298
 Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu
 70 75 80

ggg ggc gct ctg agc ctg acc ttc gtg ctg ggg ctg ctt tct ggc ttt 346
 Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser Gly Phe
 85 90 95

ttg gtc tgg aga cga tgc cgc agg aga gag aag ttc acc acc ccc ata 394
 Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile
 100 105 110

gag gag acc ggc gga gag ggc tgc cca gct gtg gcg ctg atc cag tga 442
 Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile Gln
 115 120 125

caatgtgccc cctgccagcc ggggctcgcc cactcatcat tcattcatcc attctagagc 502

cagtctctgc ctcccagacg cggcgggagc caagctcctc caaccacaag ggggggtgggg 562

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gccggtgaat cacctctgag gcctgggccc agggttcagg ggaaccttcc aagggtgtctg 622
 gttgccctgc ctctgggtcc agaacagaaa gggagcctca cgctgggtca cacaaaacag 682
 ctgacactga ctaaggaact gcagcatttg cacaggggag gggggtgccc tccttcctag 742
 aggccctggg ggccaggctg acttgggggg cagacttgac actaggcccc actcactcag 802
 atgtcctgaa attccaccac gggggtcacc ctgggggggtt agggacctat ttttaacact 862
 agaggg 868

<210> 4
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 4
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 Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly
 20 25 30
 Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
 35 40 45
 Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
 50 55 60
 Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro
 65 70 75 80
 Ile Leu Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser
 85 90 95
 Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr
 100 105 110
 Pro Ile Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile
 115 120 125
 Gln

<210> 5
 <211> 129
 <212> PRT
 <213> Mus sp.

<400> 5
 Met Ala Pro Gly Trp Pro Arg Ser Leu Pro Gln Ile Leu Val Leu Gly
 1 5 10 15
 Phe Gly Leu Val Leu Met Arg Ala Ala Ala Gly Glu Gln Ala Pro Gly
 20 25 30

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Thr Ser Pro Cys Ser Ser Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
 35 40 45
 Cys Met Asp Cys Ala Ser Cys Pro Ala Arg Pro His Ser Asp Phe Cys
 50 55 60
 Leu Gly Cys Ala Ala Ala Pro Pro Ala His Phe Arg Leu Leu Trp Pro
 65 70 75 80
 Ile Leu Gly Gly Ala Leu Ser Leu Val Leu Val Leu Ala Leu Val Ser
 85 90 95
 Ser Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr
 100 105 110
 Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Gly Val Ala Leu Ile
 115 120 125
 Gln

<210> 6
 <211> 932
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(930)
 <220>
 <223> Description of Artificial Sequence: human TWEAK
 receptor fusion protein construct

<400> 6
 atg gct cgg ggc tcg ctg cgc cgg ttg ctg cgg ctc ctc gtg ctg ggg 48
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 1 5 10 15
 ctc tgg ctg gcg ttg ctg cgc tcc gtg gcc ggg gag caa gcg cca ggc 96
 Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly
 20 25 30
 acc gcc ccc tgc tcc cgc ggc agc tcc tgg agc gcg gac ctg gac aag 144
 Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
 35 40 45
 tgc atg gac tgc gcg tct tgc agg gcg cga ccg cac agc gac ttc tgc 192
 Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
 50 55 60
 ctg ggc tgc gct gca gca cct cct gcc ccc ttc cgg ctg ctt tgg aga 240
 Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Arg
 65 70 75 80
 tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc 288

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<210> 7

<211> 309

<212> PRT

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(930)

<220>

<223> Description of Artificial Sequence: human TWEAK
receptor fusion protein construct

<400> 7

Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly
1 5 10 15Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly
20 25 30Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
35 40 45Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
50 55 60Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Arg
65 70 75 80Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
85 90 95Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
100 105 110Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
115 120 125Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
130 135 140Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
145 150 155 160Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
165 170 175Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
180 185 190Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
195 200 205

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

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210

215

220

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
225 230 235 240

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
245 250 255

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
260 265 270

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
275 280 285

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
290 295 300

Leu Ser Pro Gly Lys
305

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